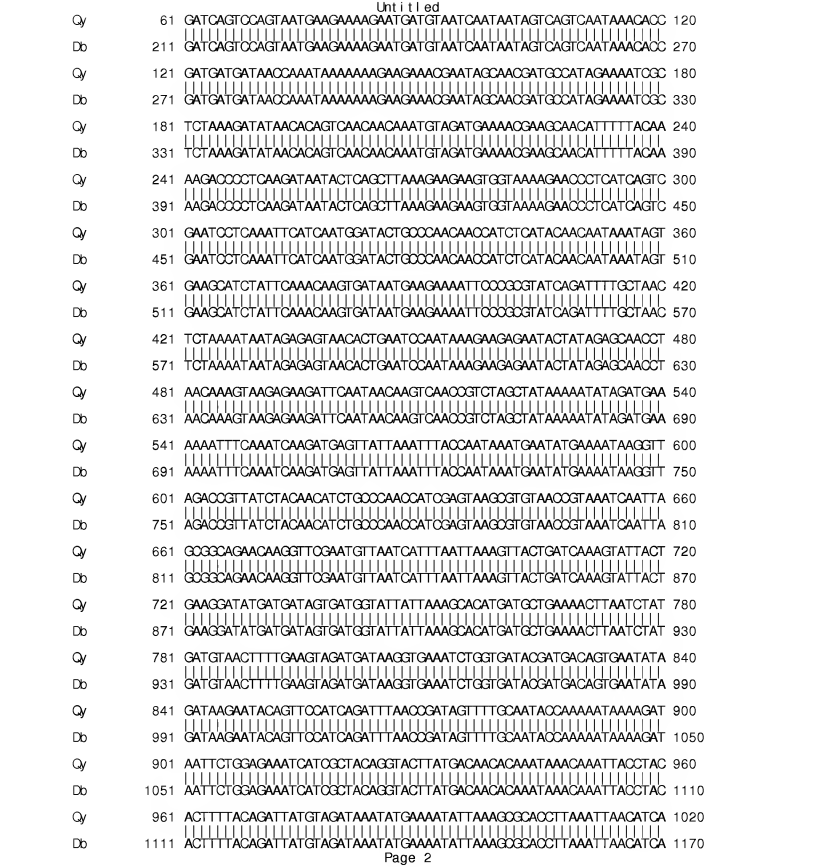
Title: US-10-615-383A-7_COPY_252_1895
Perfect score: 1644
Sequence: 1 gagaatacagtacaagacgt.....actt gcctcctgaaaaaact 1644

RESULT 3
ABN93014
ID ABN93014 standard; DNA; 2793 BP.
XX
AC ABN93014;
XX
DT 24-JUL-2002 (first entry)
XX
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:2477.
XX
KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW antibacterial; gene therapy; gene; ds.
XX
OS Staphylococcus epidermidis.
XX
PN US6380370-B1.
XX
PD 30-APR-2002.
XX
PF 13-AUG-1998; 98US-00134001.
XX
PR 14-AUG-1997; 97US-0055779P.
PR 08-NOV-1997; 97US-0064964P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Doucette-Stamm LA, Bush D;
XX
DR WPI; 2002-381255/41.
DR P-PSDB; ABP40469.
XX
PT Novel isolated nucleic acid encoding a Staphylococcus epidermis
PT polypeptide, useful for diagnosing and treating bacterial infections.
XX
PS Disclosure; SEQ ID NO 2477; 267pp; English.
XX
CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC antibacterial activity and can be used in gene therapy. The sequences can
CC also be used in the diagnosis and treatment of bacterial infections,
CC particularly S. epidermidis infections. The sequences can be used to
CC screen for compounds able to interfere with the S. epidermidis life cycle
CC or inhibit S. epidermidis infection. N.B. The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the USPTO web site
XX
SQ Sequence 2793 BP; 1149 A; 423 C; 497 G; 724 T; 0 U; 0 Other;

Query Match 100.0%; Score 1644; DB 1; Length 2793;
Best Local Similarity 100.0%
Matches 1644; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGAATACAGTACAAGACGTTAAAGATTCGAATATGGATGATGAATTATCAGATAGCAAT 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 151 GAGAATACAGTACAAGACGTTAAAGATTCGAATATGGATGATGAATTATCAGATAGCAAT 210


Qy 61 GATCAGTCCAGTAATGAAGAAAAGAATGATGTAATCAATAATAGTCAGTCAATAAACACC 120
Db 211 GATCAGTCCAGTAATGAAGAAAAGAATGATGTAATCAATAATAGTCAGTCAATAAACACC 270
Qy 121 GATGATGATAACCAAATAAAAAAAGAAGAAACGAATAGCAACGATGCCATAGAAAATCGC 180
Db 271 GATGATGATAACCAAATAAAAAAAGAAGAAACGAATAGCAACGATGCCATAGAAAATCGC 330
Qy 181 TCTAAAGATATAACACAGTCAACAACAAATGTAGATGAAAACGAAGCAACATTTTTACAA 240
Db 331 TCTAAAGATATAACACAGTCAACAACAAATGTAGATGAAAACGAAGCAACATTTTTACAA 390
Qy 241 AAGACCCCTCAAGATAATACTCAGCTTAAAGAAGAAGTGGTAAAAGAACCCTCATCAGTC 300
Db 391 AAGACCCCTCAAGATAATACTCAGCTTAAAGAAGAAGTGGTAAAAGAACCCTCATCAGTC 450
Qy 301 GAATCCTCAAAATTCATCAATGGATACTGCCCAACAACCATCTCATACAACAATAAATAGT 360
Db 451 GAATCCTCAAATTCATCAATGGATACTGCCCAACAACCATCTCATACAACAATAAATAGT 510
Qy 361 GAAGCATCTATTCAAACAAGTGATAATGAAGAAAATTCCCGCGTATCAGATTTTGCTAAC 420
Db 511 GAAGCATCTATTCAAACAAGTGATAATGAAGAAAATTCCCGCGTATCAGATTTTGCTAAC 570
Qy 421 TCTAAAATAATAGAGAGTAACACTGAATCCAATAAAGAAGAGAATACTATAGAGCAACCT 480
Db 571 TCTAAAATAATAGAGAGTAACACTGAATCCAATAAAGAAGAGAATACTATAGAGCAACCT 630
Qy 481 AACAAAGTAAGAGAAGATTCAATAACAAGTCAACCGTCTAGCTATAAAAATATAGATGAA 540
Db 631 AACAAAGTAAGAGAAGATTCAATAACAAGTCAACCGTCTAGCTATAAAAATATAGATGAA 690
Qy 541 AAAATTTCAAATCAAGATGAGTTATTAAATTTACCAATAAATGAATATGAAAATAAGGTT 600
Db 691 AAAATTTCAAATCAAGATGAGTTATTAAATTTACCAATAAATGAATATGAAAATAAGGTT 750
Qy 601 AGACCGTTATCTACAACATCTGCCCAACCATCGAGTAAGCGTGTAACCGTAAATCAATTA 660
Db 751 AGACCGTTATCTACAACATCTGCCCAACCATCGAGTAAGCGTGTAACCGTAAATCAATTA 810
Qy 661 GCGGCAGAACAAGGTTCGAATGTTAATCATTTAATTAAAGTTACTGATCAAAGTATTACT 720
Db 811 GCGGCAGAACAAGGTTCGAATGTTAATCATTTAATTAAAGTTACTGATCAAAGTATTACT 870
Qy 721 GAAGGATATGATGATAGTGATGGTATTATTAAAGCACATGATGCTGAAAACTTAATCTAT 780
Db 871 GAAGGATATGATGATAGTGATGGTATTATTAAAGCACATGATGCTGAAAACTTAATCTAT 930
Qy 781 GATGTAACTTTTGAAGTAGATGATAAGGTGAAATCTGGTGATACGATGACAGTGAATATA 840
Db 931 GATGTAACTTTTGAAGTAGATGATAAGGTGAAATCTGGTGATACGATGACAGTGAATATA 990
Qy 841 GATAAGAATACAGTTCCATCAGATTTAACCGATAGTTTTGCAATACCAAAAATAAAAGAT 900
Db 991 GATAAGAATACAGTTCCATCAGATTTAACCGATAGTTTTGCAATACCAAAAATAAAAGAT 1050
Qy 901 AATTCTGGAGAAATCATCGCTACAGGTACTTATGACAACACAAATAAACAAATTACCTAC 960
Db 1051 AATTCTGGAGAAATCATCGCTACAGGTACTTATGACAACACAAATAAACAAATTACCTAC 1110
Qy 961 ACTTTTACAGATTATGTAGATAAATATGAAAATATTAAAGCGCACCTTAAATTAACATCA 1020
Db 1111 ACTTTTACAGATTATGTAGATAAATATGAAAATATTAAAGCGCACCTTAAATTAACATCA 1170

```
Qy       1021 TACATTGATAAATCAAAGGTTCCAAATAATAACACTAAGTTAGATGTAGAATATAAGACG 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1171 TACATTGATAAATCAAAGGTTCCAAATAATAACACTAAGTTAGATGTAGAATATAAGACG 1230

Qy       1081 GCCCTTTCATCAGTAAATAAAACAATTACGGTTGAATATCAAAAACCTAACGAAAATCGG 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1231 GCCCTTTCATCAGTAAATAAAACAATTACGGTTGAATATCAAAAACCTAACGAAAATCGG 1290

Qy       1141 ACTGCTAACCTTCAAAGTATGTTCACAAACATAGATACGAAAAACCATACAGTTGAGCAA 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1291 ACTGCTAACCTTCAAAGTATGTTCACAAACATAGATACGAAAAACCATACAGTTGAGCAA 1350

Qy       1201 ACGATTTATATTAACCCTCTTCGTTATTCAGCCAAAGAAACAAATGTAAATATTTCAGGG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1351 ACGATTTATATTAACCCTCTTCGTTATTCAGCCAAAGAAACAAATGTAAATATTTCAGGG 1410

Qy       1261 AATGGCGATGAAGGTTCAACAATTATCGACGATAGTACAATCATTAAAGTTTATAAGGTT 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1411 AATGGCGATGAAGGTTCAACAATTATCGACGATAGTACAATCATTAAAGTTTATAAGGTT 1470

Qy       1321 GGAGATAATCAAAATTTACCAGATAGTAACAGAATTTATGATTACAGTGAATATGAAGAT 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1471 GGAGATAATCAAAATTTACCAGATAGTAACAGAATTTATGATTACAGTGAATATGAAGAT 1530

Qy       1381 GTCACAAATGATGATTATGCCCAATTAGGAAATAATAATGACGTGAATATTAATTTTGGT 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1531 GTCACAAATGATGATTATGCCCAATTAGGAAATAATAATGACGTGAATATTAATTTTGGT 1590

Qy       1441 AATATAGATTCACCATATATTATTAAAGTTATTAGTAAATATGACCCTAATAAGGACGAT 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1591 AATATAGATTCACCATATATTATTAAAGTTATTAGTAAATATGACCCTAATAAGGACGAT 1650

Qy       1501 TACAGGACGATACAGCAAACTGTGACAATGCAAAGGACTATAAATGAGTATACTGGTGAG 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1651 TACAGGACGATACAGCAAACTGTGACAATGCAAAGGACTATAAATGAGTATACTGGTGAG 1710

Qy       1561 TTTAGAACAGCATCCTATGATAATACAATTGCTTTCTCTACAAGTTCAGGTCAAGGACAA 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1711 TTTAGAACAGCATCCTATGATAATACAATTGCTTTCTCTACAAGTTCAGGTCAAGGACAA 1770

Qy       1621 GGTGACTTGCCTCCTGAAAAAACT 1644
             |||||||||||||||||||||||||
Db       1771 GGTGACTTGCCTCCTGAAAAAACT 1794
```

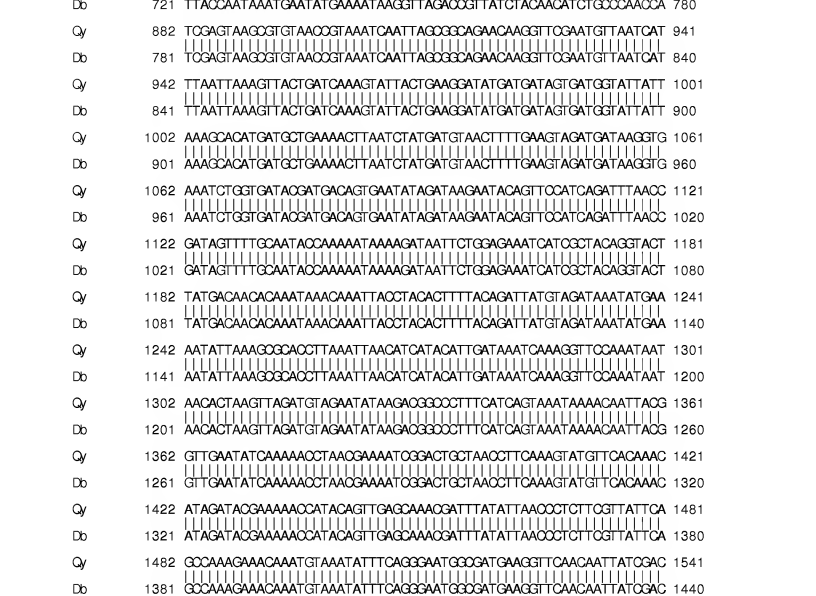
```
Title:          US-10-615-383A-7
Perfect score:  2976
Sequence:       1 atattgcaaaaaagacttat.....ccaacaaatataaggtgttg 2976
```

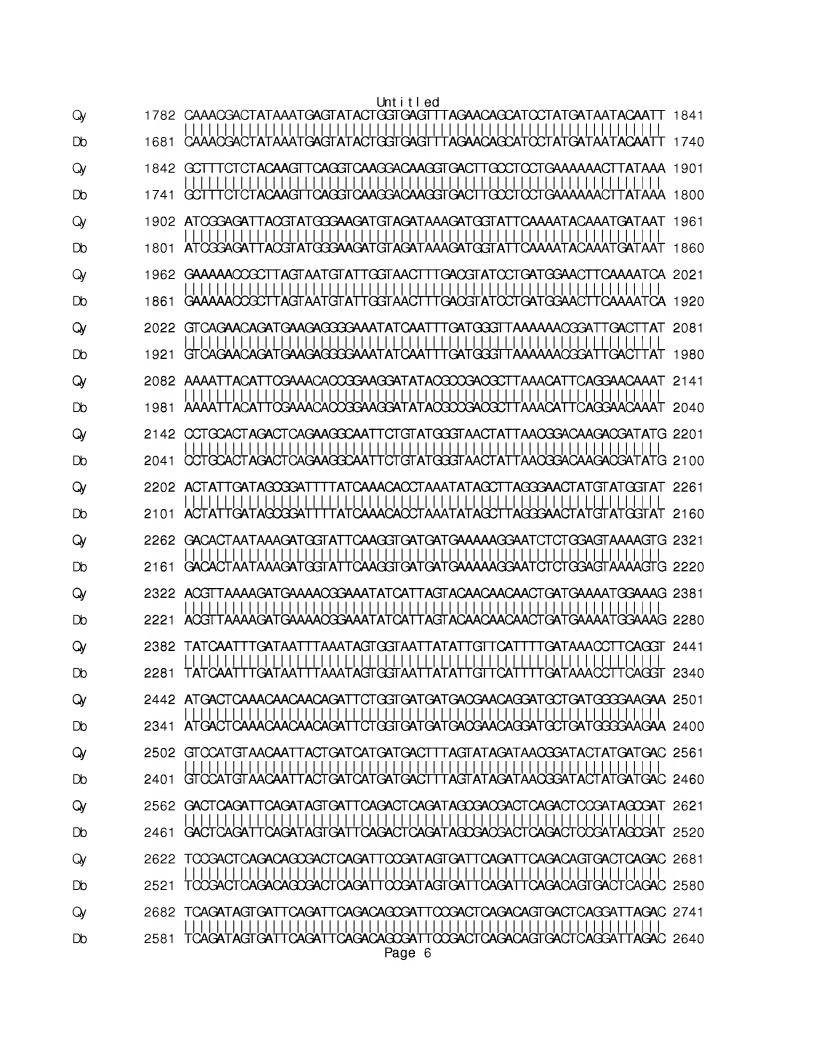
```
RESULT 4
US-09-134-001C-2477
;  Sequence 2477, Application US/09134001C
;  Patent No. 6380370
;  GENERAL INFORMATION:
;    APPLICANT: Lynn Doucette-Stamm et al
;    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLOCOCCUS
;    TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;    FILE REFERENCE: GTC-007
;    CURRENT APPLICATION NUMBER: US/09/134,001C
;    CURRENT FILING DATE:  1998-08-13
;    PRIOR APPLICATION NUMBER: US 60/064,964
```

; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2477
; LENGTH: 2793
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2477

Query Match 93.8%; Score 2791.4; DB 3; Length 2793;
Best Local Similarity 99.9%
Matches 2792; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        102 TTAAAAAAAAAATAATTTACTAACTAAAAAGAAACCTATAGCAAATAAATCCAATAAATAT 161
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTAAAAAAAAAATAATTTACTAACTAAAAAGAAACCTATAGCAAATAAATCCAATAAATAT 60

Qy        162 GCAATTAGAAAATTCACAGTAGGTACAGCGTCTATTGTAATAGGTGCAGCATTATTGTTT 221
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db         61 GCAATTAGAAAATTCACAGTAGGTACAGCGTCTATTGTAATAGGTGCAACATTATTGTTT 120

Qy        222 GGTTTAGGTCATAATGAGGCCAAAGCTGAGGAGAATACAGTACAAGACGTTAAAGATTCG 281
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGTTTAGGTCATAATGAGGCCAAAGCTGAGGAGAATACAGTACAAGACGTTAAAGATTCG 180

Qy        282 AATATGGATGATGAATTATCAGATAGCAATGATCAGTCCAGTAATGAAGAAAAGAATGAT 341
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AATATGGATGATGAATTATCAGATAGCAATGATCAGTCCAGTAATGAAGAAAAGAATGAT 240

Qy        342 GTAATCAATAATAGTCAGTCAATAAACACCGATGATGATAACCAAATAAAAAAAGAAGAA 401
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTAATCAATAATAGTCAGTCAATAAACACCGATGATGATAACCAAATAAAAAAAGAAGAA 300

Qy        402 ACGAATAGCAACGATGCCATAGAAAATCGCTCTAAAGATATAACACAGTCAACAACAAAT 461
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACGAATAGCAACGATGCCATAGAAAATCGCTCTAAAGATATAACACAGTCAACAACAAAT 360

Qy        462 GTAGATGAAAACGAAGCAACATTTTTACAAAAGACCCCTCAAGATAATACTCAGCTTAAA 521
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTAGATGAAAACGAAGCAACATTTTTACAAAAGACCCCTCAAGATAATACTCAGCTTAAA 420

Qy        522 GAAGAAGTGGTAAAAGAACCCTCATCAGTCGAATCCTCAAATTCATCAATGGATACTGCC 581
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAAGAAGTGGTAAAAGAACCCTCATCAGTCGAATCCTCAAATTCATCAATGGATACTGCC 480

Qy        582 CAACAACCATCTCATACAACAATAAATAGTGAAGCATCTATTCAAACAAGTGATAATGAA 641
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAACAACCATCTCATACAACAATAAATAGTGAAGCATCTATTCAAACAAGTGATAATGAA 540

Qy        642 GAAAATTCCCGCGTATCAGATTTTGCTAACTCTAAAATAATAGAGAGTAACACTGAATCC 701
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAAAATTCCCGCGTATCAGATTTTGCTAACTCTAAAATAATAGAGAGTAACACTGAATCC 600

Qy        702 AATAAAGAAGAGAATACTATAGAGCAACCTAACAAAGTAAGAGAAGATTCAATAACAAGT 761
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AATAAAGAAGAGAATACTATAGAGCAACCTAACAAAGTAAGAGAAGATTCAATAACAAGT 660

Qy        762 CAACCGTCTAGCTATAAAAATATAGATGAAAAAATTTCAAATCAAGATGAGTTATTAAAT 821
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAACCGTCTAGCTATAAAAATATAGATGAAAAAATTTCAAATCAAGATGAGTTATTAAAT 720

Qy        822 TTACCAATAAATGAATATGAAAATAAGGTTAGACCGTTATCTACAACATCTGCCCAACCA 881
```


Db 721 TTACCAATAAATGAATATGAAAATAAGGTTAGACCGTTATCTACAACATCTGCCCAACCA 780
Qy 882 TCGAGTAAGCGTGTAACCGTAAATCAATTAGCCGCAGAACAAGGTTCGAATGTTAATCAT 941
Db 781 TCGAGTAAGCGTGTAACCGTAAATCAATTAGCGGCAGAACAAGGTTCGAATGTTAATCAT 840
Qy 942 TTAATTAAAGTTACTGATCAAAGTATTACTGAAGGATATGATGATAGTGATGGTATTATT 1001
Db 841 TTAATTAAAGTTACTGATCAAAGTATTACTGAAGGATATGATGATAGTGATGGTATTATT 900
Qy 1002 AAAGCACATGATGCTGAAAACTTAATCTATGATGTAACTTTTGAAGTAGATGATAAGGTG 1061
Db 901 AAAGCACATGATGCTGAAAACTTAATCTATGATGTAACTTTTGAAGTAGATGATAAGGTG 960
Qy 1062 AAATCTGGTGATACGATGACAGTGAATATAGATAAGAATACAGTTCCATCAGATTTAACC 1121
Db 961 AAATCTGGTGATACGATGACAGTGAATATAGATAAGAATACAGTTCCATCAGATTTAACC 1020
Qy 1122 GATAGTTTTGCAATACCAAAAATAAAAGATAATTCTGGAGAAATCATCGCTACAGGTACT 1181
Db 1021 GATAGTTTTGCAATACCAAAAATAAAAGATAATTCTGGAGAAATCATCGCTACAGGTACT 1080
Qy 1182 TATGACAACACAAATAAACAAATTACCTACACTTTTACAGATTATGTAGATAAATATGAA 1241
Db 1081 TATGACAACACAAATAAACAAATTACCTACACTTTTACAGATTATGTAGATAAATATGAA 1140
Qy 1242 AATATTAAAGCGCACCTTAAATTAACATCATACATTGATAAATCAAAGGTTCCAAATAAT 1301
Db 1141 AATATTAAAGCGCACCTTAAATTAACATCATACATTGATAAATCAAAGGTTCCAAATAAT 1200
Qy 1302 AACACTAAGTTAGATGTAGAATATAAGACGGCCCTTTCATCAGTAAATAAAACAATTACG 1361
Db 1201 AACACTAAGTTAGATGTAGAATATAAGACGGCCCTTTCATCAGTAAATAAAACAATTACG 1260
Qy 1362 GTTGAATATCAAAAACCTAACGAAAATCGGACTGCTAACCTTCAAAGTATGTTCACAAAC 1421
Db 1261 GTTGAATATCAAAAACCTAACGAAAATCGGACTGCTAACCTTCAAAGTATGTTCACAAAC 1320
Qy 1422 ATAGATACGAAAAACCATACAGTTGAGCAAACGATTTATATTAACCCTCTTCGTTATTCA 1481
Db 1321 ATAGATACGAAAAACCATACAGTTGAGCAAACGATTTATATTAACCCTCTTCGTTATTCA 1380
Qy 1482 GCCAAAGAAACAAATGTAAATATTTCAGGGAATGGCGATGAAGGTTCAACAATTATCGAC 1541
Db 1381 GCCAAAGAAACAAATGTAAATATTTCAGGGAATGGCGATGAAGGTTCAACAATTATCGAC 1440
Qy 1542 GATAGTACAATCATTAAAGTTTATAAGGTTGGAGATAATCAAAATTTACCAGATAGTAAC 1601
Db 1441 GATAGTACAATCATTAAAGTTTATAAGGTTGGAGATAATCAAAATTTACCAGATAGTAAC 1500
Qy 1602 AGAATTTATGATTACAGTGAATATGAAGATGTCACAAATGATGATTATGCCCAATTAGGA 1661
Db 1501 AGAATTTATGATTACAGTGAATATGAAGATGTCACAAATGATGATTATGCCCAATTAGGA 1560
Qy 1662 AATAATAATGACGTGAATATTAATTTTGGTAATATAGATTCACCATATATTATTAAAGTT 1721
Db 1561 AATAATAATGACGTGAATATTAATTTTGGTAATATAGATTCACCATATATTATTAAAGTT 1620
Qy 1722 ATTAGTAAATATGACCCTAATAAGGACGATTACACGACGATACAGCAAACTGTGACAATG 1781
Db 1621 ATTAGTAAATATGACCCTAATAAGGACGATTACACGACGATACAGCAAACTGTGACAATG 1680


Qy 1782 CAAACGACTATAAATGAGTATACTGGTGAGTTTAGAACAGCATCCTATGATAATACAATT 1841
Db 1681 CAAACGACTATAAATGAGTATACTGGTGAGTTTAGAACAGCATCCTATGATAATACAATT 1740
Qy 1842 GCTTTCTCTACAAGGTTCAGGTCAAGCACAAGGTGACTTGCCTCCTGAAAAAACTTATAAA 1901
Db 1741 GCTTTCTCTACAAGGTTCAGGTCAAGGACAAGGTGACTTGCCTCCTGAAAAAACTTATAAA 1800
Qy 1902 ATCGGAGATTACGTATGGGAAGATGTAGATAAAGATGGTATTCAAAATACAAATGATAAT 1961
Db 1801 ATCGGAGATTACGTATGGGAAGATGTAGATAAAGATGGTATTCAAAATACAAATGATAAT 1860
Qy 1962 GAAAAACCGCTTAGTAATGTATTGGTAACTTTGACGTATCCTGATGGAACTTCAAAATCA 2021
Db 1861 GAAAAACCGCTTAGTAATGTATTGGTAACTTTGACGTATCCTGATGGAACTTCAAAATCA 1920
Qy 2022 GTCAGAACAGATGAAGAGGGGAAATATCAATTTGATGGGTTAAAAAACGGATTGACTTAT 2081
Db 1921 GTCAGAACAGATGAAGAGGGGAAATATCAATTTGATGGGTTAAAAAACGGATTGACTTAT 1980
Qy 2082 AAAATTACATTCGAAACACCGGAAGGATATACGCCGACGCTTAAACATTCAGGAACAAAT 2141
Db 1981 AAAATTACATTCGAAACACCGGAAGGATATACGCCGACGCTTAAACATTCAGGAACAAAT 2040
Qy 2142 CCTGCACTAGACTCAGAAGGCAATTCTGTATGGGTAACTATTAACGGACAAGACGATATG 2201
Db 2041 CCTGCACTAGACTCAGAAGGCAATTCTGTATGGGTAACTATTAACGGACAAGACGATATG 2100
Qy 2202 ACTATTGATAGCGGATTTTATCAAACACCTAAATATAGCTTAGGGAACTATGTATGGTAT 2261
Db 2101 ACTATTGATAGCGGATTTTATCAAACACCTAAATATAGCTTAGGGAACTATGTATGGTAT 2160
Qy 2262 GACACTAATAAAGATGGTATTCAAGGTGATGATGAAAAAGGAATCTCTGGAGTAAAAGTG 2321
Db 2161 GACACTAATAAAGATGGTATTCAAGGTGATGATGAAAAAGGAATCTCTGGAGTAAAAGTG 2220
Qy 2322 ACGTTAAAAGATGAAAACGGAAATATCATTAGTACAACAACAACTGATGAAAATGGAAAG 2381
Db 2221 ACGTTAAAAGATGAAAACGGAAATATCATTAGTACAACAACAACTGATGAAAATGGAAAG 2280
Qy 2382 TATCAATTTGATAATTTAAATAGTGGTAATTATATTGTTCATTTTGATAAACCTTCAGGT 2441
Db 2281 TATCAATTTGATAATTTAAATAGTGGTAATTATATTGTTCATTTTGATAAACCTTCAGGT 2340
Qy 2442 ATGACTCAAACAACAACAGATTCTGGTGATGATGACGAACAGGATGCTGATGGGGAAGAA 2501
Db 2341 ATGACTCAAACAACAACAGATTCTGGTGATGATGACGAACAGGATGCTGATGGGGAAGAA 2400
Qy 2502 GTCCATGTAACAATTACTGATCATGATGACTTTAGTATAGATAACGGATACTATGATGAC 2561
Db 2401 GTCCATGTAACAATTACTGATCATGATGACTTTAGTATAGATAACGGATACTATGATGAC 2460
Qy 2562 GACTCAGATTCAGATAGTGATTCAGACTCAGATAGCGACGACTCAGACTCCGATAGCGAT 2621
Db 2461 GACTCAGATTCAGATAGTGATTCAGACTCAGATAGCGACGACTCAGACTCCGATAGCGAT 2520
Qy 2622 TCCGACTCAGACAGCGACTCAGATTCCGATAGTGATTCAGATTCAGACAGTGACTCAGAC 2681
Db 2521 TCCGACTCAGACAGCGACTCAGATTCCGATAGTGATTCAGATTCAGACAGTGACTCAGAC 2580
Qy 2682 TCAGATAGTGATTCAGATTCAGACAGCGATTCCGACTCAGACAGTGACTCAGGATTAGAC 2741
Db 2581 TCAGATAGTGATTCAGATTCAGACAGCGATTCCGACTCAGACAGTGACTCAGGATTAGAC 2640

```
Qy        2742 AATAGCTCAGATAAGAATACAAAAGATAAATTACCGGATACAGGAGCTAATGAAGATCAT 2801
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2641 AATAGCTCAGATAAGAATACAAAAGATAAATTACCGGATACAGGAGCTAATGAAGATCAT 2700

Qy        2802 GATTCTAAAGGCACATTACTTGGAGCTTTATTTGCAGGTTTAGGAGCGTTATTATTAGGG 2861
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2701 GATTCTAAAGGCACATTACTTGGAGCTTTATTTGCAGGTTTAGGAGCGTTATTATTAGGG 2760

Qy        2862 AAGCGTCGCAAAAATAGAAAAAATAAAAATTAA 2894
               ||||||||||||||||||||||||||||||||
Db        2761 AAGCGTCGCAAAAATAGAAAAAATAAAAATTAA 2793

Title:          US-10-615-383A-10
Perfect score:  4824
Sequence:       1 LKKNNLLTKKKPIANKSNKY.....FAGLGALLLGKRRKNRKNKN 930


RESULT 3
ABP40469
ID   ABP40469 standard; protein; 930 AA.
XX
AC   ABP40469;
XX
DT   24-JUL-2002  (first entry)
XX
DE   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5314.
XX
KW   Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW   antibacterial; gene therapy.
XX
OS   Staphylococcus epidermidis.
XX
PN   US6380370-B1.
XX
PD   30-APR-2002.
XX
PF   13-AUG-1998;    98US-00134001.
XX
PR   14-AUG-1997;    97US-0055779P.
PR   08-NOV-1997;    97US-0064964P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Doucette-Stamm LA,  Bush D;
XX
DR   WPI; 2002-381255/41.
DR   N-PSDB; ABN93014.
XX
PT   Novel isolated nucleic acid encoding a Staphylococcus epidermis
PT   polypeptide, useful for diagnosing and treating bacterial infections.
XX
PS   Disclosure; SEQ ID NO:5314; 267pp; English.
XX
CC   ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC   frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC   given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC   antibacterial activity and can be used in gene therapy. The sequences can
CC   also be used in the diagnosis and treatment of bacterial infections,
CC   particularly S. epidermidis infections. The sequences can be used to
CC   screen for compounds able to interfere with the S. epidermidis life cycle
CC   or inhibit S. epidermidis infection. N.B. The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
```

CC in electronic format directly from the USPTO web site

XX

SQ Sequence 930 AA;

Query Match 99.9%; Score 4820; DB 1; Length 930;
Best Local Similarity 99.9%;
Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          841 SDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSGLDNSSDKNTKDKLPDTGANEDH 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 SDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSGLDNSSDKNTKDKLPDTGANEDH 900

Qy          901 DSKGTLLGALFAGLGALLLGKRRKNRKNKN 930
                |||||||||||||||||||||||||||||
Db          901 DSKGTLLGALFAGLGALLLGKRRKNRKNKN 930


Title:          US-10-615-383A-10_COPY_51_598
Perfect score:  2808
Sequence:       1 ENTVQDVKDSNMDDELSDSN.........TIAFSTSSGQGQGDLPPEKT 548
```

```
RESULT 4
ABP40469
ID   ABP40469 standard; protein; 930 AA.
XX
AC   ABP40469;
XX
DT   24-JUL-2002  (first entry)
XX
DE   Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5314.
XX
KW   Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW   antibacterial; gene therapy.
XX
OS   Staphylococcus epidermidis.
XX
PN   US6380370-B1.
XX
PD   30-APR-2002.
XX
PF   13-AUG-1998;    98US-00134001.
XX
PR   14-AUG-1997;    97US-0055779P.
PR   08-NOV-1997;    97US-0064964P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
PI   Doucette-Stamm LA,  Bush D;
XX
DR   WPI; 2002-381255/41.
DR   N-PSDB; ABN93014.
XX
PT   Novel isolated nucleic acid encoding a Staphylococcus epidermis
PT   polypeptide, useful for diagnosing and treating bacterial infections.
XX
PS   Disclosure; SEQ ID NO 5314; 267pp; English.
XX
CC   ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC   frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC   given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC   antibacterial activity and can be used in gene therapy. The sequences can
CC   also be used in the diagnosis and treatment of bacterial infections,
CC   particularly S. epidermidis infections. The sequences can be used to
CC   screen for compounds able to interfere with the S. epidermidis life cycle
CC   or inhibit S. epidermidis infection. N.B. The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from the USPTO web site
XX
```

SQ Sequence 930 AA;

Query Match 100.0%; Score 2808; DB 1; Length 930;
Best Local Similarity 100.0%
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    1 ENTVQDVKDSNVDDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENR 60
Db   51 ENTVQDVKDSNVDDELSDSNDQSSNEEKNDVINNSQSINTDDDNQIKKEETNSNDAIENR 110

Qy   61 SKDITQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSVDTAQQPSHTTINS 120
Db  111 SKDITQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSVDTAQQPSHTTINS 170

Qy  121 EASIQTSDNEENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDE 180
Db  171 EASIQTSDNEENSRVSDFANSKIIESNTESNKEENTIEQPNKVREDSITSQPSSYKNIDE 230

Qy  181 KISNQDELLNLPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSIT 240
Db  231 KISNQDELLNLPINEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLIKVTDQSIT 290

Qy  241 EGYDDSDGIIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKD 300
Db  291 EGYDDSDGIIKAHDAENLIYDVTFEVDDKVKSGDTMTVNIDKNTVPSDLTDSFAIPKIKD 350

Qy  301 NSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKT 360
Db  351 NSGEIIATGTYDNTNKQITYTFTDYVDKYENIKAHLKLTSYIDKSKVPNNNTKLDVEYKT 410

Qy  361 ALSSVNKTITVEYGKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISG 420
Db  411 ALSSVNKTITVEYGKPNENRTANLQSMFTNIDTKNHTVEQTIYINPLRYSAKETNVNISG 470

Qy  421 NGDEQSTIIDDSTIIKVYKVGDNQNLPDSNRIYDYSEYEVDTNDDYAQLGNNNDVNIFG 480
Db  471 NGDEQSTIIDDSTIIKVYKVGDNQNLPDSNRIYDYSEYEVDTNDDYAQLGNNNDVNIFG 530

Qy  481 NIDSPYIIKVISKYDPNKDDYTTICQTVTMQTTINEYTGEFRTASYDNTIAFSTSSGQSQ 540
Db  531 NIDSPYIIKVISKYDPNKDDYTTICQTVTMQTTINEYTGEFRTASYDNTIAFSTSSGQSQ 590

Qy  541 GDLPPEKT 548
Db  591 GDLPPEKT 598
```